

10.511719

! DT01 Rec'd OCT 18 OCT 2004

SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of β ig- h 3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 10

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

<400> 1

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 20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
 35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
 50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
 65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
 85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
 100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
 115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
 130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val

145	150	155	160
Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val			
165	170	175	
Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr			
180	185	190	
Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly			
195	200	205	
Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala			
210	215	220	
Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr			
225	230	235	240
Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu			
245	250	255	
Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn			
260	265	270	
Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile			
275	280	285	
Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg			
290	295	300	
Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala			
305	310	315	320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu			
325	330	335	
Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile			
340	345	350	
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp			
355	360	365	
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala			
370	375	380	
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu			
385	390	395	400

Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
 405 410 415
 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
 420 425 430
 Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
 435 440 445
 Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
 450 455 460
 Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
 465 470 475 480
 Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
 485 490 495
 Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
 500 505 510
 Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
 515 520 525
 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
 530 535 540
 Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
 545 550 555 560
 Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
 565 570 575
 Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
 580 585 590
 Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
 595 600 605
 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
 610 615 620
 Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
 625 630 635 640
 Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
 645 650 655

Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
 660 665 670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
 675 680

<210> 2
 <211> 2691
 <212> DNA
 <213> Homo sapiens

<400> 2
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 ccgccaagtc gccctaccag ctggtgctgc agcacagcag gctccggggc cgccagcacg 180
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 atcctaattg gattgtaact gtgaactgtg cccggctcct gaaagccgac caccatgcaa 720
 ccaacggggg ggtgcacctc atcgataagg tcatctccac catcaccaac aacatccagc 780
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 tcgagaagat ccctagttag actttgaacc gtatcctggg cgaccagaa gccctgagag 960
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tccatgtcat caccaatgtt ctgcagctc cagccaacag acctcaggaa agaggggatg	1980
aacttcgaga ctctgcgctt gagatcttca aacaagcatc agcgttttcc agggcttccc	2040
agaggtctgt gcgactagcc cctgtctatc aaaagttatt agagaggatg aagcattagc	2100
ttgaagcact acaggaggaa tgcaccacgg cagctctccg ccaatttctc tcagatttcc	2160
acagagactg tttgaatgtt ttcaaaacca agtatcacac tttaatgtac atgggccgca	2220
ccataatgag atgtgagcct tgtgcatgtg ggggaggagg gagagagatg tactttttaa	2280
atcatgttcc ccctaaacat ggctgttaac ccactgcatg cagaaacttg gatgtcactg	2340
cctgacattc acttccagag aggacctatc ccaaagtgtg aattgactgc ctatgccaag	2400

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tccctggaaa aggagcttca gtattgtggg gtcataaaa catgaatcaa gcaatccagc      2460
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attataagct atgagttgaa atgttctgtc aaatgtgtct cacatctaca cgtggcttgg      2580
aggcttttat ggggccctgt ccaggtagaa aagaaatggt atgtagagct tagatttccc      2640
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<210>      3
<211>      585
<212>      PRT
<213>      Homo sapiens

<220>
<221>      PEPTIDE
<222>      (1)..(585)
<223>      69 to 653 amino acid sequence of human ID No.1

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Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr
      35             40             45

Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met
      50             55             60

Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp
      65             70             75             80

Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn
      85             90             95

Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val
      100            105            110

Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln
      115            120            125

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Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val
 130 135 140

Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val
 145 150 155 160

Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln
 165 170 175

Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val
 180 185 190

Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr
 195 200 205

Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr
 210 215 220

Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn
 225 230 235 240

Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly
 245 250 255

Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser
 260 265 270

Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp
 275 280 285

Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile
 290 295 300

Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val
 305 310 315 320

Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu
 325 330 335

Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe
 340 345 350

Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg
 355 360 365

Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly
 370 375 380

Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr
 385 390 395 400

Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys
 405 410 415

Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro
 420 425 430

Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser
 435 440 445

Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn
 450 455 460

Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg
 465 470 475 480

Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu
 485 490 495

Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser
 500 505 510

Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys
 515 520 525

Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro
 530 535 540

Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile
 545 550 555 560

Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp
 565 570 575

Glu Leu Ala Asp Ser Ala Leu Glu Ile
 580 585

<210> 4
 <211> 1857
 <212> DNA
 <213> Mouse Intracisternal A-particle

<400> 4

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cagcacggcc ccaatgtatg tgctgtgcag aaggtcattg gcaccaacaa gaaatacttc	120
accaactgca agcagtggta ccagaggaag atctgcggca agtcgacagt catcagttat	180
gagtgtctgc ctggatatga aaaggtocca ggagagaaag gttgcccagc agctcttccg	240
ctctcaaadc tgtatgagac catggggagtt gtgggatcga ccaccacaca gctgtataca	300
gaccgcacag aaaagctgag gcctgagatg gagggacccg gaagcttcac catctttgct	360
cctagcaatg aggcctggtc ttccttgccct gcggaagtgc tggactccct ggtgagcaac	420
gtcaacatcg aactgctcaa tgctctccgc taccacatgg tggacaggcg ggtcctgacc	480
gatgagctca agcacggcat gaccctcacc tccatgtacc agaattccaa catccagatc	540
catcactatc ccaatgggat tgtaactgtt aactgtgccc ggctgctgaa ggctgaccac	600
catgcgacca acggcgtggt gcatctcatt gacaaggctc tttccaccat caccaacaac	660
atccagcaga tcattgaaat cgaggacacc ttgagacac ttcgggcccgc cgtggctgca	720
tcaggactca ataccgtgct ggagggcgac ggccagtcca cactcttggc cccaaccaac	780
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ctgagagacc tgctaaacaa ccacatcctg aagtcagcca tgtgtgctga ggccattgta	900
gctggaatgt ccatggagac cctggggggc accacactgg aggtgggctg cagtggggac	960
aagetcacca tcaacgggaa ggctgtcatc tccaacaaag acatcctggc caccaacggt	1020
gtcattcatt tcattgatga gctgcttacc ccagattcag ccaagacact gcttgagctg	1080
gctggggaat ctgacgtctc cactgccatt gacatcctca aacaagctgg cctcgatact	1140
catctctctg ggaaagaaca gttgaccttc ctggccccc tgaattctgt gttcaaagat	1200
gggtgccctc gcatcgacgc ccagatgaag actttgcttc tgaaccacat ggtcaaagaa	1260
cagttggcct ccaagtatct gtactctgga cagacactgg acacgctggg tggcaaaaag	1320
ctgcgagtct ttgtttatcg aaatagcctc tgcattgaaa acagctgcat tgctgcccac	1380
gataagaggg gacgggtttg gaccctgttc accatggacc ggatgttgac accccaatg	1440

gggacagtta tggatgtcct gaagggagac aatcgtttta gcatgctggt ggccgccatc 1500
 cagtctgcag gactcatgga gatcctcaac cggaagggg tctacactgt ttttgcctcc 1560
 accaatgaag cgttccaagc catgcctcca gaagaactga acaaactctt ggcaaagtcc 1620
 aaggaactta ccaacatcct gaagtaccac attggtgatg aaatcctggt tagcggaggc 1680
 atcgggggccc tgggtgggct gaagtctctc caaggggaca aactggaagt cagctcgaaa 1740
 aacaatgtag tgagtgtcaa taaggagcct gttgccgaaa ccgacatcat ggccacaaac 1800
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<210> 5
 <211> 609
 <212> PRT
 <213> Mouse Intracisternal A-particle

 <220>
 <221> PEPTIDE
 <222> (1)..(609)
 <223> 23 to 641 amino acid sequence of mouse

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 Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
 20 25 30
 Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
 35 40 45
 Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
 50 55 60
 Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
 65 70 75 80
 Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
 85 90 95
 Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly

100	105	110
Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser		
115	120	125
Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu		
130	135	140
Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr		
145	150	155
160		
Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser		
165	170	175
Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys		
180	185	190
Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His		
195	200	205
Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile		
210	215	220
Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val Ala Ala		
225	230	235
240		
Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr Leu Leu		
245	250	255
Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr Leu Asn		
260	265	270
Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn Asn His		
275	280	285
Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly Leu Ser		
290	295	300
Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser Gly Asp		
305	310	315
320		
Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp Ile Leu		
325	330	335
Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile Pro Asp		
340	345	350

Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val Ser Thr
355 360 365

Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu Ser Gly
370 375 380

Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe Lys Asp
385 390 395 400

Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg Asn His
405 410 415

Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly Gln Thr
420 425 430

Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr Arg Asn
435 440 445

Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys Arg Gly
450 455 460

Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro Pro Met
465 470 475 480

Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu
485 490 495

Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu
500 505 510

Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu
515 520 525

Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala
530 535 540

Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly
545 550 555 560

Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu
565 570 575

Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala
580 585 590

Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn
595 600 605

Val

<210> 6
 <211> 391
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> β ig-h3 D-IV

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 ccaagccatg cctccagaag aactgaacaa actcttggca aatgccaagg aacttaccaa 240
 catcctgaag taccacattg gtgatgaaat cctgggttagc ggaggcatcg gggccctggt 300
 gcggctgaag tctctccaag gggacaaact ggaagtcagc tcgaaaaaca atgtagttag 360
 tgtcaataag gagcctgttg ccgaaaccga c 391

<210> 7
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> β ig-h3 D-IV(1X) amino acid sequence

<400> 7
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 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu

35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
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 115 120 125
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
 130 135 140

<210> 8
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> β ig-h3 D-IV(2X) amino acid sequence

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 1 5 10 15
 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln

85	90	95
Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn		
100	105	110
Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val		
115	120	125
His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro		
130	135	140
Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met		
145	150	155
Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg		
165	170	175
Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala		
180	185	190
Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu		
195	200	205
Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly		
210	215	220
Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu		
225	230	235
Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val		
245	250	255
Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr		
260	265	270
Asn Val Leu Gln Pro Pro Ala Asn		
275	280	

<210> 9
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> β ig-h3 D-IV(3X) amino acid sequence

<400> 9

Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
 1 5 10 15

Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30

Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45

Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60

Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80

Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95

Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110

Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125

His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 130 135 140

Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 145 150 155 160

Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 165 170 175

Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 180 185 190

Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 195 200 205

Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
 210 215 220

Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 225 230 235 240

Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 245 250 255

Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
 260 265 270

Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
 275 280 285

Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
 290 295 300

Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr
 305 310 315 320

Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
 325 330 335

Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
 340 345 350

Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
 355 360 365

Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
 370 375 380

Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
 385 390 395 400

Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln
 405 410 415

Pro Pro Ala Asn
 420

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 <211> 560
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> β ig-h3 D-IV(4X) amino acid sequence

<400> 10

Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
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 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110
 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 130 135 140
 Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 145 150 155 160
 Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 165 170 175
 Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 180 185 190
 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 195 200 205
 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
 210 215 220
 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 225 230 235 240
 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 245 250 255

Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
260 265 270

Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
275 280 285

Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
290 295 300

Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr
305 310 315 320

Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
325 330 335

Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
340 345 350

Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
355 360 365

Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
370 375 380

Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
385 390 395 400

Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln
405 410 415

Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu
420 425 430

Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala
435 440 445

Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala
450 455 460

Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg
465 470 475 480

Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile
485 490 495

Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu

500	505	510
Lys Ser Leu Gln Gly Asp	Lys Leu Glu Val Ser Leu Lys Asn Asn Val	
515	520	525
Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr		
530	535	540
Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn		
545	550	555 560